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TECH CENTER 1600/2900

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/714,882

DATE: 05/29/2001
TIME: 11:46:13

Input Set : **A:\Seqlist.txt**
Output Set: **C:\CRF3\05292001\I714882.raw**

ENTERED

```
 4 <110> APPLICANT: Turner, C. Alexander Jr.
 5        Nehls, Michael C.
 6        Friedrich, Glenn
 7        Zambrowicz, Brian
 8        Sands, Arthur T.
10 <120> TITLE OF INVENTION: Novel Human Notch Ligand Proteins and Polynucleotides
11        Encoding the Same
13 <130> FILE REFERENCE: LEX-0091-USA
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/714,882
C--> 15 <141> CURRENT FILING DATE: 2000-11-16
15 <150> PRIOR APPLICATION NUMBER: US 60/165,959
16 <151> PRIOR FILING DATE: 1999-11-17
18 <160> NUMBER OF SEQ ID NOS: 14
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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23 <211> LENGTH: 2070
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <400> SEQUENCE: 1
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30 gtgaacgaaa tcaaacaata tttatcacac atattggaac aaagaacatc tagtaatgta       180
31 atcaataaaa gagaaaatct·cctggagaaa aagaagaatc aacgtaaaat aagaataaaa       240
32 ggaattcaaa ataaagatat cttgaagaga aataagaatc atttacaaaa gcaagcagag       300
33 aaaaatttta cagatgaagg agaccagcta tttaagatgg gcatcaaggt tctccagcag       360
34 tctaaaagcc aaaaacaaaa agaagaagcc tacctacttt ttgccaaagc agctgacatg       420
35 ggaaacttga aagctatgga gaaaatggct gacgctttgc tatttggaaa ttttggcgtg       480
36 caaaatataa cagcagctat ccaattatat gagtccttgg ctaaagaagg atcatgtaaa       540
37 gcccaaaacg cattaggatt tttgtcttct tatggaatag gaatggaata tgatcaagct       600
38 aaggcactga tatattacac ctttggaagt gctggaggaa acatgatgtc ccagatgatt       660
39 ttggggtaca gatatttgtc gggaatcaat gttctacaga attgtgaagt tgccctaagt       720
40 tattacaaga aagtggcaga ttatattgct gacacatttg aaaaaagtga aggtgttcca       780
41 gtggaaaaag tgagactaac ggaaagacct gaaaatctga gttctaacag tgagattttg       840
42 gattgggaca tataccaata ctataaattt ttggcagaaa gaggagatgt tcagatacaa       900
43 gtctctcttg acaattaca tctaattggc aggaaaggtc tagatcagga ttactacaaa       960
44 gcattacact acttcttaaa ggcagcaaag gccgggagtg caaatgccat ggcatttata      1020
45 ggaaagatgt atttagaggg gaatgctgcc gtgccgcaaa ataacgctac tgccttcaag      1080
46 tactttt cca tggcagccag taagggcaat gcaatcggcc ttcatgggct tggtcttctt      1140
47 tactttcatg aaaaggagt tcccctgaat tatgccraag cacttaaata ctttcagaaa      1200
48 gctgcggaaa aagggtggcc cgacgcacag ttccagttag gcttcatgta ctactctggc      1260
49 tctggaatat ggaaggatta taaacttgcc ttcaaatatt tttacctggc atctcagagt      1320
50 gggcagcccc tcgccattta ttatctggcc aagatgtatg caacaggaac aggagtagta      1380
51 agatcatgca gaactgctgt ggagctttat aaaggtgtct gtgaactagg ccactgggct      1440
52 gagaaattcc tgacagctta ctttgcctat aaggatggtg atatagattc ttctcttgtt      1500
53 cagtatgcac tgcttgcaga atgggggtat gaagtagctc aaagcaattc agcattcatt       1560
54 ttggaatcta aaaaggctaa cattcttgaa aaagagaaga tgtatccaat ggcgcttctc      1620
55 ctatggaatc gagctgccat tcaaggcaat gcatttgcta gagtaaaaat tggagattac      1680
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PATENT APPLICATION: US/09/714,882

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56 cattactatg gctatgggac taagaaagac tatcaaacag cagccacaca ctacagcatt    1740
57 gcagccaaca aataccacaa cgcgcaagcc atgttcaatc tggcttatat gtatgaacac    1800
58 ggcttaggca tcacaaagga cattcacttg gccagaagat tgtacgacat ggctgctcaa    1860
59 acgagtccag atgcccacat acctgtgctc tttgccgtca tgaaactgga aactacgcat    1920
60 ttgctccggg atatcctgtt ttttaatcag ttcacaacga gatggaactg gctgaaactg    1980
61 gacaacacca ttggaccaca ctgggactta tttgtgattg gcctcattgt tcctgggctg    2040
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64 <210> SEQ ID NO: 2
65 <211> LENGTH: 689
66 <212> TYPE: PRT
67 <213> ORGANISM: Homo sapiens
69 <400> SEQUENCE: 2
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71 1               5                   10                  15
72 Thr Ile Lys Thr Ile Lys Ala Glu Glu His Asn Lys Arg Gln Lys Glu
73              20                  25                  30
74 Arg Asn Val Thr Thr Gln Val Ser Val Asn Glu Ile Lys Gln Tyr Leu
75              35                  40                  45
76 Ser His Ile Leu Glu Gln Arg Thr Ser Ser Asn Val Ile Asn Lys Arg
77      50                  55                  60
78 Glu Asn Leu Leu Glu Lys Lys Lys Asn Gln Arg Lys Ile Arg Ile Lys
79 65               70                  75                  80
80 Gly Ile Gln Asn Lys Asp Ile Leu Lys Arg Asn Lys Asn His Leu Gln
81              85                  90                  95
82 Lys Gln Ala Glu Lys Asn Phe Thr Asp Glu Gly Asp Gln Leu Phe Lys
83              100                 105                 110
84 Met Gly Ile Lys Val Leu Gln Gln Ser Lys Ser Gln Lys Gln Lys Glu
85              115                 120                 125
86 Glu Ala Tyr Leu Leu Phe Ala Lys Ala Ala Asp Met Gly Asn Leu Lys
87      130                 135                 140
88 Ala Met Glu Lys Met Ala Asp Ala Leu Leu Phe Gly Asn Phe Gly Val
89 145              150                 155                 160
90 Gln Asn Ile Thr Ala Ala Ile Gln Leu Tyr Glu Ser Leu Ala Lys Glu
91              165                 170                 175
92 Gly Ser Cys Lys Ala Gln Asn Ala Leu Gly Phe Leu Ser Ser Tyr Gly
93              180                 185                 190
94 Ile Gly Met Glu Tyr Asp Gln Ala Lys Ala Leu Ile Tyr Tyr Thr Phe
95              195                 200                 205
96 Gly Ser Ala Gly Gly Asn Met Met Ser Gln Met Ile Leu Gly Tyr Arg
97      210                 215                 220
98 Tyr Leu Ser Gly Ile Asn Val Leu Gln Asn Cys Glu Val Ala Leu Ser
99 225                  230                 235                 240
100 Tyr Tyr Lys Lys Val Ala Asp Tyr Ile Ala Asp Thr Phe Glu Lys Ser
101                 245                 250                 255
102 Glu Gly Val Pro Val Glu Lys Val Arg Leu Thr Glu Arg Pro Glu Asn
103                 260                 265                 270
104 Leu Ser Ser Asn Ser Glu Ile Leu Asp Trp Asp Ile Tyr Gln Tyr Tyr
105                 275                 280                 285
106 Lys Phe Leu Ala Glu Arg Gly Asp Val Gln Ile Gln Val Ser Leu Gly
```

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107     290                 295                 300
108 Gln Leu His Leu Ile Gly Arg Lys Gly Leu Asp Gln Asp Tyr Tyr Lys
109 305                 310                 315                 320
110 Ala Leu His Tyr Phe Leu Lys Ala Ala Lys Ala Gly Ser Ala Asn Ala
111             325                 330                 335
112 Met Ala Phe Ile Gly Lys Met Tyr Leu Glu Gly Asn Ala Ala Val Pro
113             340                 345                 350
114 Gln Asn Asn Ala Thr Ala Phe Lys Tyr Phe Ser Met Ala Ala Ser Lys
115             355                 360                 365
116 Gly Asn Ala Ile Gly Leu His Gly Leu Gly Leu Leu Tyr Phe His Gly
117     370                 375                 380
118 Lys Gly Val Pro Leu Asn Tyr Ala Glu Ala Leu Lys Tyr Phe Gln Lys
119 385                 390                 395                 400
120 Ala Ala Glu Lys Gly Trp Pro Asp Ala Gln Phe Gln Leu Gly Phe Met
121             405                 410                 415
122 Tyr Tyr Ser Gly Ser Gly Ile Trp Lys Asp Tyr Lys Leu Ala Phe Lys
123             420                 425                 430
124 Tyr Phe Tyr Leu Ala Ser Gln Ser Gly Gln Pro Leu Ala Ile Tyr Tyr
125             435                 440                 445
126 Leu Ala Lys Met Tyr Ala Thr Gly Thr Gly Val Val Arg Ser Cys Arg
127     450                 455                 460
128 Thr Ala Val Glu Leu Tyr Lys Gly Val Cys Glu Leu Gly His Trp Ala
129 465                 470                 475                 480
130 Glu Lys Phe Leu Thr Ala Tyr Phe Ala Tyr Lys Asp Gly Asp Ile Asp
131             485                 490                 495
132 Ser Ser Leu Val Gln Tyr Ala Leu Leu Ala Glu Met Gly Tyr Glu Val
133             500                 505                 510
134 Ala Gln Ser Asn Ser Ala Phe Ile Leu Glu Ser Lys Lys Ala Asn Ile
135             515                 520                 525
136 Leu Glu Lys Glu Lys Met Tyr Pro Met Ala Leu Leu Leu Trp Asn Arg
137     530                 535                 540
138 Ala Ala Ile Gln Gly Asn Ala Phe Ala Arg Val Lys Ile Gly Asp Tyr
139 545                 550                 555                 560
140 His Tyr Tyr Gly Tyr Gly Thr Lys Lys Asp Tyr Gln Thr Ala Ala Thr
141             565                 570                 575
142 His Tyr Ser Ile Ala Ala Asn Lys Tyr His Asn Ala Gln Ala Met Phe
143             580                 585                 590
144 Asn Leu Ala Tyr Met Tyr Glu His Gly Leu Gly Ile Thr Lys Asp Ile
145             595                 600                 605
146 His Leu Ala Arg Arg Leu Tyr Asp Met Ala Ala Gln Thr Ser Pro Asp
147     610                 615                 620
148 Ala His Ile Pro Val Leu Phe Ala Val Met Lys Leu Glu Thr Thr His
149 625                 630                 635                 640
150 Leu Leu Arg Asp Ile Leu Phe Phe Asn Gln Phe Thr Thr Arg Trp Asn
151             645                 650                 655
152 Trp Leu Lys Leu Asp Asn Thr Ile Gly Pro His Trp Asp Leu Phe Val
153             660                 665                 670
154 Ile Gly Leu Ile Val Pro Gly Leu Ile Leu Leu Leu Arg Asn His His
155     675                 680                 685
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   Input Set : **A:\Seqlist.txt**
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156 Gly
159 <210> SEQ ID NO: 3
160 <211> LENGTH: 2067
161 <212> TYPE: DNA
162 <213> ORGANISM: Homo sapiens
164 <400> SEQUENCE: 3
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166 atcaaagcag aggaacataa taaaagacaa aaggaaagaa atgtcaccac acaggtatca    120
167 gtgaacgaaa tcaaacaata tttatcacac atattggaac aaagaacatc tagtaatgta    180
168 atcaataaaa gagaaaatct cctggagaaa aagaagaatc aacgtaaaat aagaataaaa    240
169 ggaattcaaa ataaagatat cttgaagaga aataagaatc atttacaaaa gcaagcagag    300
170 aaaaatttta cagatgaagg agaccagcta tttaagatgg gcatcaaggt tctccagcag    360
171 tctaaaagcc aaaaacaaaa agaagaagcc tacctacttt ttgccaaagc agctgacatg    420
172 ggaaacttga aagctatgga gaaaatggct gacgctttgc tatttggaaa ttttggcgtg    480
173 caaaatataa cagcagctat ccaattatat gagtccttgg ctaaagaagg atcatgtaaa    540
174 gcccaaaacg cattaggatt tttgtcttct tatggaatag gaatggaata tgatcaagct    600
175 aaggcactga tatattacac ctttggaagt gctggaggaa acatgatgtc ccagatgatt    660
176 ttggggtaca gatatttgtc gggaatcaat gttctacaga attgtgaagt tgccctaagt    720
177 tattacaaga aagtggcaga ttatattgct gacacatttg aaaaaagtga aggtgttcca    780
178 gtggaaaaag tgagactaac ggaaagacct gaaaatctga gttctaacag tgagattttg    840
179 gattgggaca tataccaata ctataaattt ttggcagaaa gaggagatgt tcagatacaa    900
180 gtctctcttg gacaattaca tctaattggc aggaaaggtc tagatcagga ttactacaaa    960
181 gcattacact acttcttaaa ggcagcaaag gccgggagtg caaatgccat ggcatttata   1020
182 ggaaagatgt atttagaggg gaatgctgcc gtgccgcaaa ataacgctac tgccttcaag   1080
183 tacttttcca tggcagccag taagggcaat gcaatcggcc ttcatgggct tggtcttctt   1140
184 tactttcatg gaaaaggagt tcccctgaat tatgccraag cacttaaata ctttcagaaa   1200
185 gctgcggaaa aagggtggcc cgacgcacag ttccagttag gcttcatgta ctactctggc   1260
186 tctggaatat ggaaggatta taaacttgcc ttcaaatatt tttacctggc atctcagagt   1320
187 gggcagcccc tcgccattta ttatctggcc aagatgtatg caacaggaac aggagtagta   1380
188 agatcatgca gaactgctgt ggagctttat aaaggtgtct gtgaactagg ccactgggct   1440
189 gagaaattcc tgacagctta ctttgcctat aaggatggtg atatagattc ttctcttgtt   1500
190 cagtatgcac tgcttgcaga aatggggtat gaagtagctc aaagcaattc agcattcatt   1560
191 ttggaatcta aaaaggctaa cattcttgaa aaagagaaga tgtatccaat ggcgcttctc   1620
192 ctatggaatc gagctgccat tcaaggcaat gcatttgcta gagtaaaaat tggagattac   1680
193 cattactatg gctatgggac taagaaagac tatcaaacag cagccacaca ctacagcatt   1740
194 gcagccaaca ataccacaa cgcgcaagcc atgttcaatc tggcttatat gtatgaacac   1800
195 ggcttaggca tcacaaagga cattcacttg ccagaagat gtacgacat ggctgctcaa   1860
196 acgagtccag atgcccacat acctgtgctc tttgccgtca tgaaactgga aactacgcat   1920
197 ttgctccggg atatcctgtt ttttaatttc acaacgagat ggaactggct gaaactggac   1980
198 aacaccattg gaccacactg ggacttattt gtgattggcc tcattgttcc tgggctgatt   2040
199 ttgttgctta gaaatcacca tgggtag                                       2067
201 <210> SEQ ID NO: 4
202 <211> LENGTH: 688
203 <212> TYPE: PRT
204 <213> ORGANISM: Homo sapiens
206 <400> SEQUENCE: 4
207 Met Lys Pro Leu Ser Leu Leu Ile Glu Ile Leu Ile Ile Leu Gly Val
208 1               5                   10                  15
209 Thr Ile Lys Thr Ile Lys Ala Glu Glu His Asn Lys Arg Gln Lys Glu
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210              20              25              30
211 Arg Asn Val Thr Thr Gln Val Ser Val Asn Glu Ile Lys Gln Tyr Leu
212        35              40              45
213 Ser His Ile Leu Glu Gln Arg Thr Ser Ser Asn Val Ile Asn Lys Arg
214        50              55              60
215 Glu Asn Leu Leu Glu Lys Lys Lys Asn Gln Arg Lys Ile Arg Ile Lys
216 65              70              75              80
217 Gly Ile Gln Asn Lys Asp Ile Leu Lys Arg Asn Lys Asn His Leu Gln
218              85              90              95
219 Lys Gln Ala Glu Lys Asn Phe Thr Asp Glu Gly Asp Gln Leu Phe Lys
220        100             105             110
221 Met Gly Ile Lys Val Leu Gln Gln Ser Lys Ser Gln Lys Gln Lys Glu
222        115             120             125
223 Glu Ala Tyr Leu Leu Phe Ala Lys Ala Ala Asp Met Gly Asn Leu Lys
224        130             135             140
225 Ala Met Glu Lys Met Ala Asp Ala Leu Leu Phe Gly Asn Phe Gly Val
226 145             150             155             160
227 Gln Asn Ile Thr Ala Ala Ile Gln Leu Tyr Glu Ser Leu Ala Lys Glu
228             165             170             175
229 Gly Ser Cys Lys Ala Gln Asn Ala Leu Gly Phe Leu Ser Ser Tyr Gly
230             180             185             190
231 Ile Gly Met Glu Tyr Asp Gln Ala Lys Ala Leu Ile Tyr Tyr Thr Phe
232        195             200             205
233 Gly Ser Ala Gly Gly Asn Met Met Ser Gln Met Ile Leu Gly Tyr Arg
234        210             215             220
235 Tyr Leu Ser Gly Ile Asn Val Leu Gln Asn Cys Glu Val Ala Leu Ser
236 225             230             235             240
237 Tyr Tyr Lys Lys Val Ala Asp Tyr Ile Ala Asp Thr Phe Glu Lys Ser
238             245             250             255
239 Glu Gly Val Pro Val Glu Lys Val Arg Leu Thr Glu Arg Pro Glu Asn
240        260             265             270
241 Leu Ser Ser Asn Ser Glu Ile Leu Asp Trp Asp Ile Tyr Gln Tyr Tyr
242        275             280             285
243 Lys Phe Leu Ala Glu Arg Gly Asp Val Gln Ile Gln Val Ser Leu Gly
244        290             295             300
245 Gln Leu His Leu Ile Gly Arg Lys Gly Leu Asp Gln Asp Tyr Tyr Lys
246 305             310             315             320
247 Ala Leu His Tyr Phe Leu Lys Ala Ala Lys Ala Gly Ser Ala Asn Ala
248             325             330             335
249 Met Ala Phe Ile Gly Lys Met Tyr Leu Glu Gly Asn Ala Ala Val Pro
250        340             345             350
251 Gln Asn Asn Ala Thr Ala Phe Lys Tyr Phe Ser Met Ala Ala Ser Lys
252        355             360             365
253 Gly Asn Ala Ile Gly Leu His Gly Leu Gly Leu Leu Tyr Phe His Gly
254        370             375             380
255 Lys Gly Val Pro Leu Asn Tyr Ala Glu Ala Leu Lys Tyr Phe Gln Lys
256 385             390             395             400
257 Ala Ala Glu Lys Gly Trp Pro Asp Ala Gln Phe Gln Leu Gly Phe Met
258             405             410             415
```

VERIFICATION SUMMARY   DATE: 05/29/2001
PATENT APPLICATION: **US/09/714,882**   TIME: 11:46:14

Input Set : **A:\Seqlist.txt**
Output Set: **C:\CRF3\05292001\I714882.raw**

L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date